

1/6

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Figure 1b

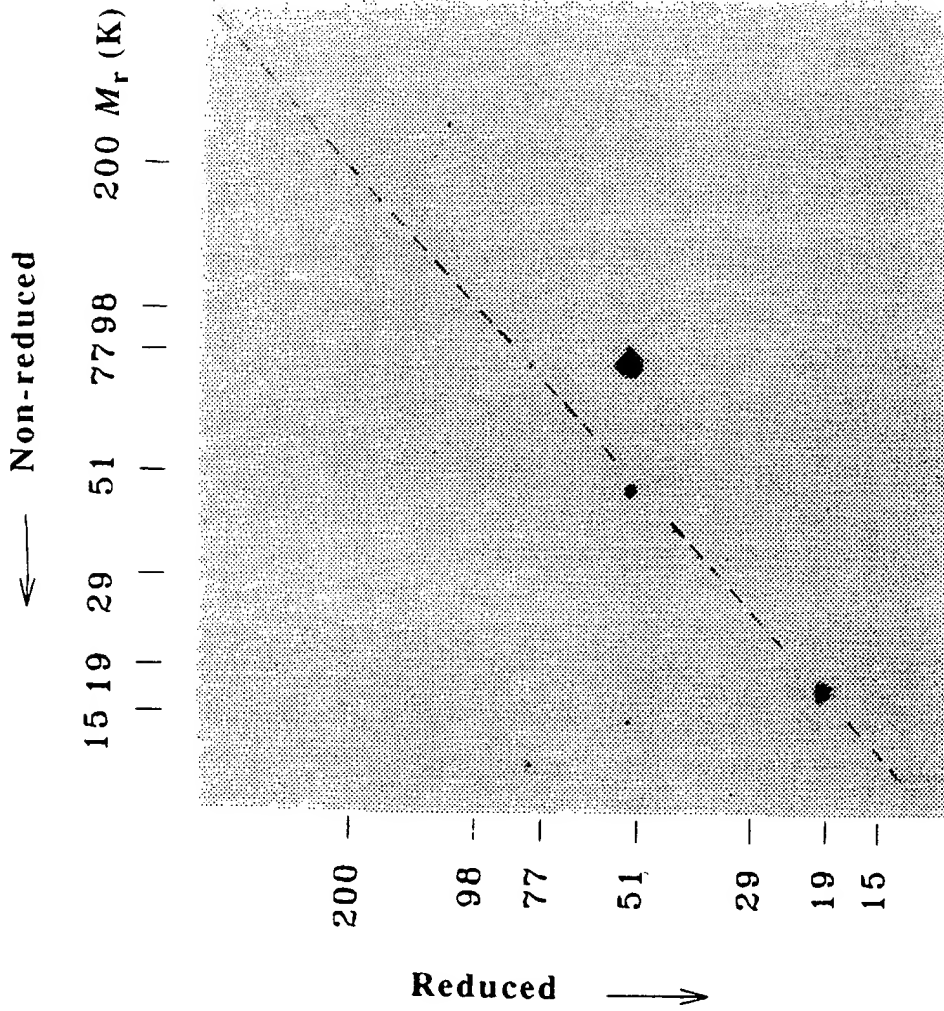
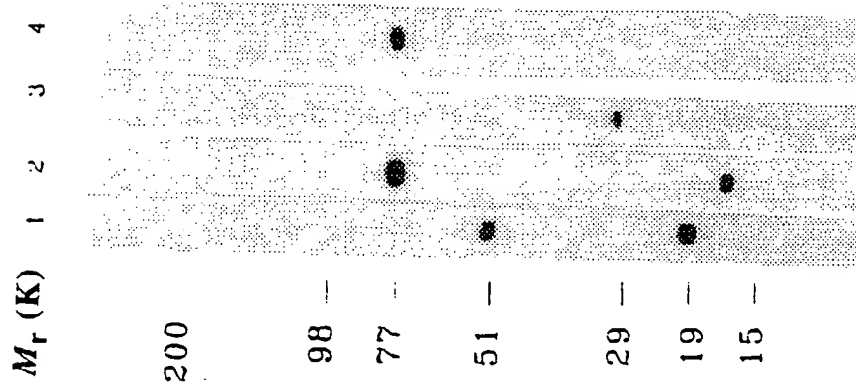


Figure 1a



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2/6

Figure 2

— C1r/C1s —>		
MASP-2	TPLGPKWPEPVFGRSLASPGFPGEYANDQERRWTLTAPPGYRLRLYFTHFDLELSHLCEYDFVKLSSGAKVLATLGEQESTDTERAPGKDT	90
MASP-1	HTVELNNMFGQIQSPGYPSDSEVTWNITVPDGFRIKLYFMHFNLESSYLCEYDYVKVETEDQVLATFGRETTDTETPGQEV	87
C1r	SIIPIQKLFGEVTSPLFPKPYNNFETTTVITVPTGYRVKLVFQQFDLEPSEGGFYDYVKISADKKSLGRPGQLGSLGNPPGKKE	87
C1s	EPTMYGEILSPNYPQAYPSEVEKSWDIEVPEGYGIHLFYTHLDIELSENCAVDSVQIIISGDTEEGRLGQRSSNNPHSPIVEE	83
* * * * *		
EGF —>		
MASP-2	FYSLGSSLDITFRSDYSNEKP FTGFEAFYAAEDIDEQ VAPGEA PTCDDHCHNHLGGFYSCRAGYVLHRNKRTCSALCS	170
MASP-1	VLSPGSFMSITFRSDFSNEER FTGFDAYMAVDVDECK EREDEE LSCDHYCHNYIGGYYSCSRFGYILHTDNRTSRVECS	167
C1r	FMSQGNKMLLTFTHDFSNEENGTFMYKGFLLAYQAVDLDEASRSKSGEEDPQPOQHLCNHYVGGYFSCSRPGYELQEDRHSQAECS	177
C1s	FQVPYNKLQVIFKSDFSNEER FTGFAAYVATDINECT DFVD VPQSHFQNNFIGGYFSCSPPPEYFLHDDMKNEGVNCS	161
* * * * *		
— C1r/C1s —>		
MASP-2	GQVFTQSGELSSPEYPRPYPKLSSCTYSISLEEGFSVILDFV ESPDVT HPETLCOPYDFLKIQTDRREEHGGPFGKTLPHR IETKS	256
MASP-1	DNLFTQRTGVTSPDFPNPYPKSSECLYTIELEEGFMVNLOFE DIFDIED HPEVPCOPYDYIKIKVGPVKLGPFGGEKAPEP ISTQS	253
C1r	SELYTEASGYISSLEYPRSYPPDLRCNYSIRVERGLTLHLKFL BPFDDID HQQVHCOPYDQLQIYANGKNIGEFQKQRPDP LDTSS	263
C1s	GDVFTALIGEIASPNYPKPYPENSRCQYQIRLEKGFQVVVTLRREDFDVEAADSAGNC LDSLVFVAGDRQFGPYCGHGFPGPLNIETKS	250
* * * * *		
CCP-1 —>		
MASP-2	NTVTITFVTDSEGDHTGKWIHYTSTAQPCPYPMAPPN GHVSPVQAKYILKDSFSIFCETGYELLQGHLPKLSFTAVQCKDGSWDRPMPA	345
MASP-1	HSVLILFHSNDNGENRGWRLSYRAAGNECPQLPPVH GKIEPSQAKYFFKDQVLVSCDTGYKVLKDNVEMDTFQIECLDKGTWSNKIPT	342
C1r	NAVDLLFFTDSEGDSRGWKLRYTTEIIEKPPQKTLDEFTIIQNLPQYQFRDYFIATCKQGYQLIEGNQVLHSFTAVQDDGTWHRAMPR	353
C1s	NALDIIFQTDLTGQKKGWKLRYHGDPMPCPKEDTPN SVWEPAKAKYVFRDVVQITCLDGFVEVGRVGATSFYSTCQSNKGWSNSKLK	338
* * * * *		
CCP-2 —>		
MASP-2	ESIVDEGPPDDLPSGRVEYITGPGVTTYKAVIQYSCETFYTM K VNDGKYVCEADGEFTSSKGEKSLPVCEPVGGLS ARTT	426
MASP-1	EKIVDGRAPGELEHGLITFSTRNNLTYYKSEIKYSCQEPYKML NNNTGIYTCQAQGVMMNKVLGRSLPTCLPVGGLPKFSRKL	426
C1r	EKIKDGGQPRNLPNGDFRYTTTGMVNTYKARIQYCHEPYKMQTRAGSRESEQGVYTTAQGIWKNEQKGEKIPRELFPVGGKPVNPFVEQ	443
C1s	QOPVDGIPESIEKVE DPESTLFGSVIRYTCPEPYMYE NGGGGEYHCAGNGSWVNEVLGPPELPKCVPVGVPREPFE	419
* * * * *		
serine protease —>		
MASP-2	GGRIYGGQKAKPGDFPWQVLILGGTTA AGALLYDNWVLTAAH AVYEQKHDASALDIRMGTLLKRLSPHYTQAWSEAVFIHEG	507
MASP-1	MARIFNGRPAQKGTTPWIAMLSHLNQPFQGGSLGSSWIVTAAHCLHQSLDPKDPPTLRSDLLSPSD FKIIIGKHWRLSRSDENEQHLG	515
C1r	RQRIIGGQKAKMGNFPWQVFTNIHGRG GGALLGDRWILTAAH TLYPKEHEAQSNASLDVFLGHTNVEELMKLGNHP IRRV	523
C1s	KQRIIGGSADAIKNFPWQVFDNPWA GGALINEYVWLTAAH VVEGNREPTMYVGSTSVQTSRLAKSKMLT PEHVFIHPG	498
* * * * *		
FDNDIALIKLNKVVINSNITPICLPKEAESFMRTDDIGTASGWGLTQRGFLARNLMYVDIPVDHQKATAAYEK		589
MASP-2	YTHDAG	
MASP-1	VKHTTLHPKYDPNTFENDVALVELLESFVLNAPVMPICLP EGPQOEGAMVIVSGWGKQFLQRFPETLMIEIPIVDHSTOKAY	599
C1r	SVHPDYRQDESYN FEGDIALLELENSVTLGPNLLPICLP DNDTFYDLGLMGYVSGFGVMEEK IAHDLRFVRLPVANPQACEN WLR	608
C1s	WKLEEV PEGRTN FDNDIALVRLKDPVKMGPTVSPICLPGTSSDYNLMDGLGLISGWGRTEKRDRAVRLKAARLPVAPLRKEKVEKVE	586
* * * * *		
PPYPRG SVTANMLCAGLESQKDSRGDSGGALVFLDS ETERWVGGIVSWGSMNCGEAGQYGVYTKVINIYIPWIENIISDF		671
MASP-2		
MASP-1	APLKK KVTRDMICAGEKEGGKDAESGDSGGPMVTLNR ERGQWYLVGTVSWGD DCGKKDRYGVYSYIHHNKDWIQRVTGVRN	680
C1r	GKNRMD VFSQNMFCAGHPSLKQDAQOGDSGGVFAVRDP NTDRAWATGIVSWG I GQSRG YGFYTKVLNVYDWMIKKEMEED	688
C1s	KPTADAEAYVTFPNMICAGGEK GMDSCKGDSSGAFVQDPNDKTKFYAAGLVSWGP QCGT YGLYTRVKNVYDWMIKMTQENSTPRED	673
* * * * *		

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3/6 Figure 3a

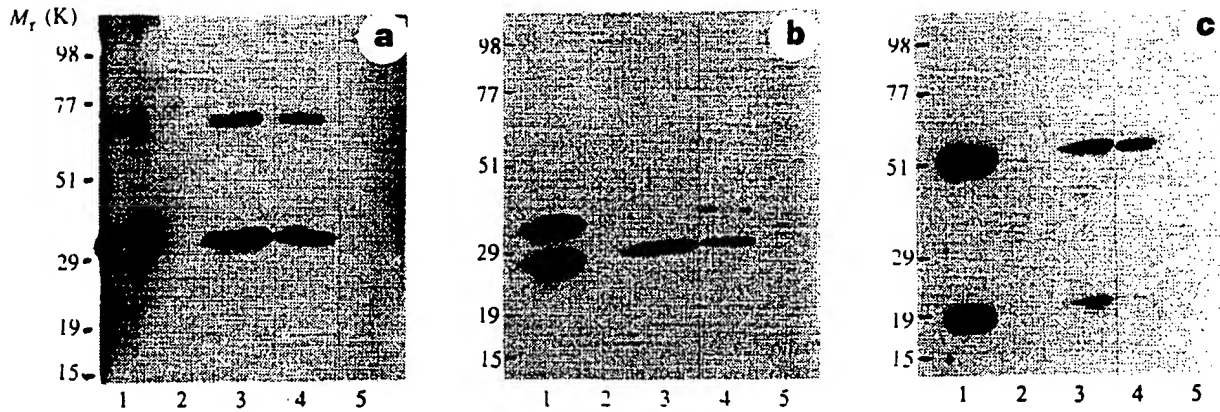
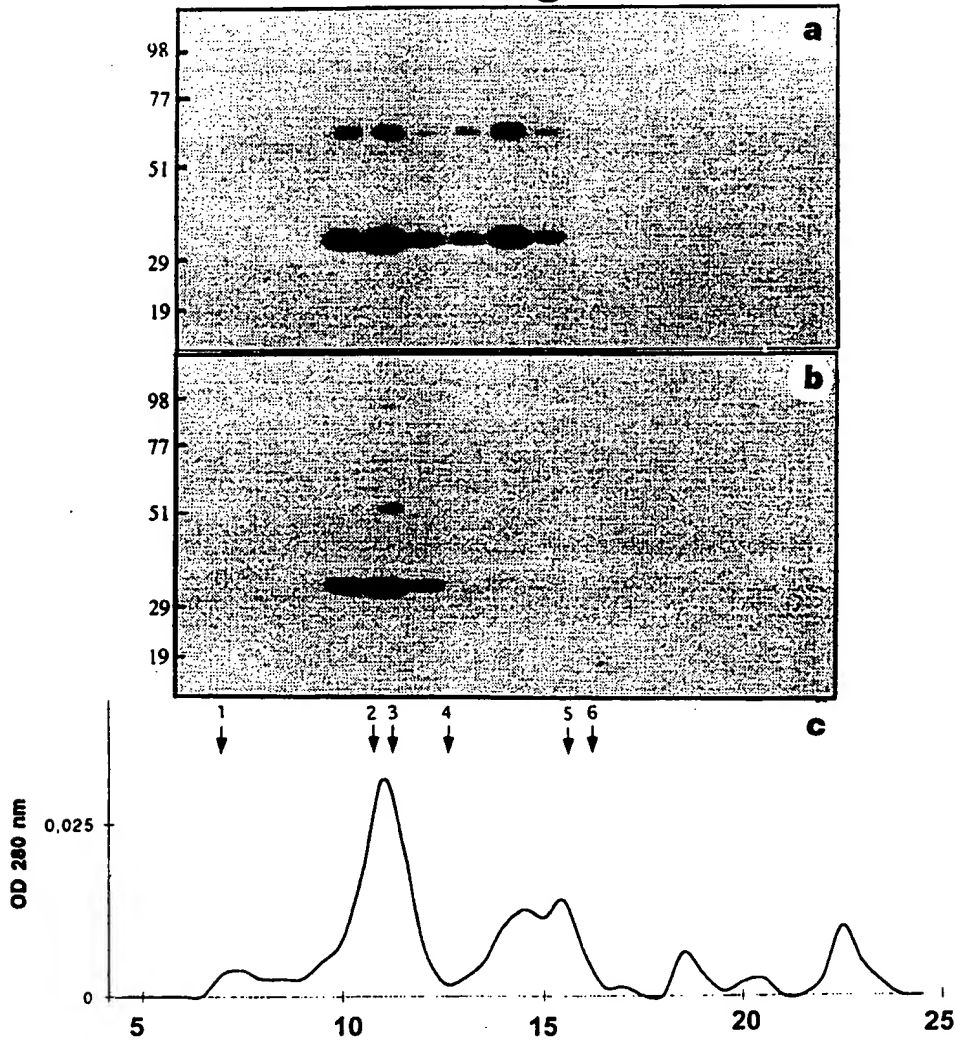


Figure 3b



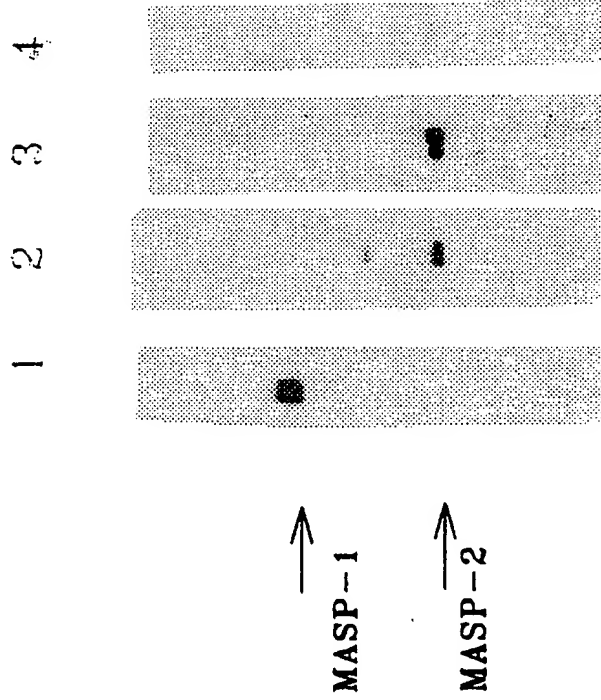
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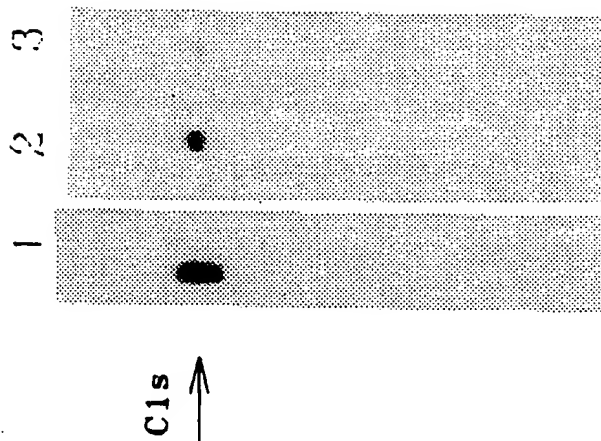
4/6

Figure 4

Blot of MBL preparation

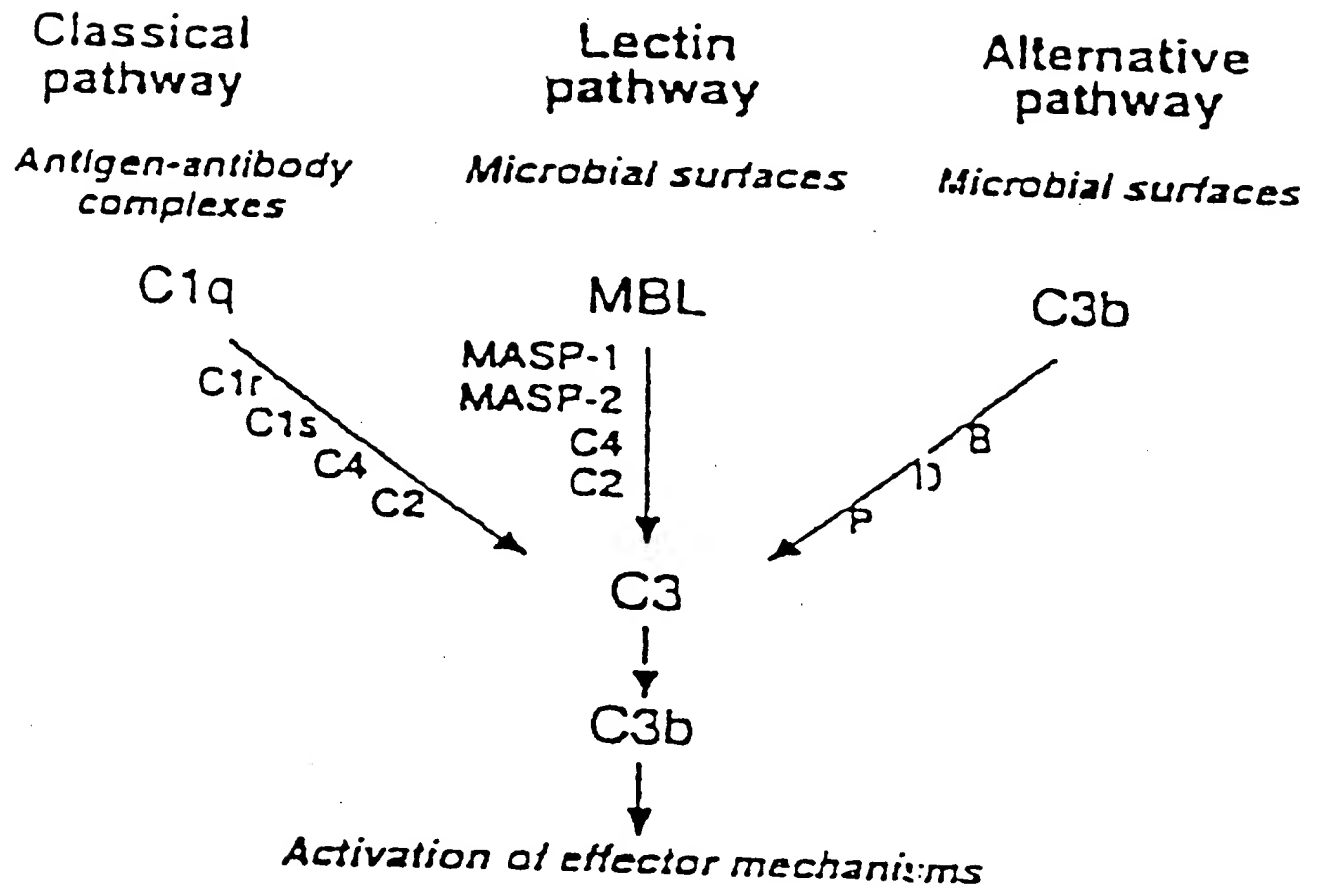


Blot of C1



5/6

Figure 5



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6/6

Figure 6

ctcgtgcaattcgggacgagggctggaggggacaccATGAGGCTGCTCACCCTCCTGGGCTTCTGTGTGCTCGGTGGCCACCCCTTAGGCCGGAAGT 100
M R L L T L L G L L C G S V A T P L G P K 6
GGCCTGAACCTGTGTTGGGGCGCTGGCATCCCCGGCTTTCAGGGGAGTATGCCAATGACCAGGAGCGGCGCTGGACCTGACTGCACCCCCGGCTA 200
W P E P V F G R L A S P G F P G E Y A N D O E R R W T L T A P P G Y 40
CGCCCTGGCCTCTACTTCACCCACTTCGACCTGGAGCTCTCCACCTCTGCGAGTACGACTTCGTCAAGCTGAGCTCGGGGGCCAGGTGCTGGCCAG 300
R L R L Y F T H F D L E L S H L C E Y D F V K L S S G A K V L A T 73
CTGTGCGGGCAGGAGAGCACAGACCGGAGCGGGCCCCCTGGCAAGGACACTTCTACTCGCTGGGCTCCTGCGTGGACATTACCTTCGCTCCGACTACT 400
L C Q E S T D T E R A P G K D T F Y S L G S S L D I T F R S D Y 106
CCAAAGGAAAGCGCTTCAGGGGTTTCAGGGCTTCTATGACGCGAGGACATTACGAGTCCGAGTCCGAGTCCGAGGAGGCGCCCACTGCGGACCA 500
S N E K P P T G F E A F Y A A E D I D E C Q V I P G E A P T C D H H 140
CCACACCCACTCGGGGGTTTCTACTGCTCCTGCGCGCGAGGCTACGTCCTGACCGTAACAGCGGACCTGCTCAGCCCTGTGCTCGGGCCAGGTC 600
C H N H L G G F Y C S C R A G Y V L H R N X R T C S A L C S G Q V 173
TTCACCCAGAGGTCTGGGAGCTCAGCAGCCCTGAATACCCAGGCGGTATCCCAACTCTCAGTTGCTCTTACAGCATCAGCCTGGAGGAGGGGTTCA 700
F-T Q R S G E L S S P E Y P R P Y P K L S S C T Y S I S L E E G F 206
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S V I L D F V E S F D V E T H P E T L C P Y D P L K I O T D R E E H 240
TGGCCCATCTGTGCGAAGACATTGCCCCACAGGATTGAAACAAAGGCAACCGGTACCATCCTTGTGCAAGATGAATCAGGAGACCAACAGGC 900
G P F C G K T L P H R I E T K S N T V T I T F V T D E S G D H T G 273
TOGAAGATCCACTACAGGACACAGCGCAGCCTTGGCTTATCCGATGGCGCACTAATGGCCAGTTTCACCTGTGCAAGCCAAATACATCTGAAAG 1000
W K I H Y T S T A Q P C P Y P M A P P N G H V S P V Q A K Y I L K 306
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D S F S I F C E T T G Y E L L Q G H L P L K S F T A V C Q K D G S W D 340
CGGGCCATGCGCGCTCAGCATTGTGACTGTGCGCTCCTGATGATCTACCCAGTGGCGGAGTGGATACATCAGGTCTGAGGTGACCACCTAC 1200
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